

#2
OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/843,377

DATE: 05/14/2001
 TIME: 09:23:55

Input Set : A:\RTS-0235 Sequence Listing.txt
 Output Set: N:\CRF3\05142001\I843377.raw

ENTERED

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6 <110> APPLICANT: C. Frank Bennett
7   Andrew T. Watt
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 2 EXPRESSION
11 <130> FILE REFERENCE: RTS-0235
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/843,377
C--> 13 <141> CURRENT FILING DATE: 2001-04-26
13 <160> NUMBER OF SEQ ID NOS: 89
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17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
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29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
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42 <210> SEQ ID NO: 3
43 <211> LENGTH: 2214
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
48 <221> NAME/KEY: CDS
49 <222> LOCATION: (649)...(1662)
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54 atcccgatctc aaaaaaaagg ggaggggggc gggggagagt tgaaagctta atatgtactt 120
56 tgggggctat taaagcaaac atttcgacta aagggggcga tcctcgaatt gtgcgtatcaa 180
58 gaccccgaga ggagagttgg ggggggtcag gagggggtggg ggctccaggg aacggccggg 240
60 ggcctgggcc ggggtctcgc gggcccttc cggaaaggatc gcgccccccg aagggtggcg 300
62 tccccgggg ctccagtcgc caggacgttc cgggaggctc cgcgctctgg gaggccggct 360
64 gctgtgggtc cccgcgcgtc agccgcagag gccccccagg gccgcgggtc ccggagcggg 420
66 aaagtcccgcc gccccggcgg tggccctcggg ggcgggacgg ggcggggcgc gggggcgggg 480
68 cggccgagcc gaatcccttc caccgggacg ccccgctgcc gctcgggaaag aggcgggccc 540
70 tgcgcgcctt gcgctcgcca tggcggtttg ggcggcgcacg tgagcggttc cgccggacccc 600
72 gagcggggcc cccgcgcga cctgagccgc cggcgagcgc cccggggcc atg cga ccg 657
73                                         Met Arg Pro
74                                         1
76 acg ctg ctg tgg tgg ctg ctg ctg ctc gga gtc ttc gcc gcc gcc 705
77 Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe Ala Ala Ala
78      5          10          15

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80	gcc	gcg	gcc	ccg	cca	gac	cct	tcc	cag	ctg	ccc	gct	cct	cag	cac		753		
81	Ala	Ala	Ala	Pro	Pro	Asp	Pro	Leu	Ser	Gln	Leu	Pro	Ala	Pro	Gln	His			
82	20					25				30						35			
84	ccg	aag	att	cgc	ctg	tac	aac	gca	gag	cag	gtc	ctg	agt	tgg	gag	cca		801	
85	Pro	Lys	Ile	Arg	Leu	Tyr	Asn	Ala	Glu	Gln	Val	Leu	Ser	Trp	Glu	Pro			
86						40				45						50			
88	gtg	gcc	ctg	agc	aat	agc	acg	agg	cct	gtt	gtc	tac	cga	gtg	cag	ttt		849	
89	Val	Ala	Leu	Ser	Asn	Ser	Thr	Arg	Pro	Val	Val	Tyr	Arg	Val	Gln	Phe			
90						55				60						65			
92	aaa	tac	acc	gac	agt	aaa	tgg	ttc	acg	gcc	gac	atc	atg	tcc	ata	ggg		897	
93	Lys	Tyr	Thr	Asp	Ser	Lys	Trp	Phe	Thr	Ala	Asp	Ile	Met	Ser	Ile	Gly			
94						70				75						80			
96	gtg	aat	tgt	aca	cag	atc	aca	gca	aca	gag	tgt	gac	ttc	act	gcc	gcc		945	
97	Val	Asn	Cys	Thr	Gln	Ile	Thr	Ala	Thr	Glu	Cys	Asp	Phe	Thr	Ala	Ala			
98						85				90						95			
100	agt	ccc	tca	gca	ggc	ttc	cca	atg	gat	ttc	aat	gtc	act	cta	cgc	ttt		993	
101	Ser	Pro	Ser	Ala	Gly	Phe	Pro	Met	Asp	Phe	Asn	Val	Thr	Leu	Arg	Leu			
102	100					105					110						115		
104	cga	gct	gag	ctg	gga	gca	ctc	cat	tct	gcc	tgg	gtg	aca	atg	cct	tgg		1041	
105	Arg	Ala	Glu	Leu	Gly	Ala	Leu	His	Ser	Ala	Trp	Val	Thr	Met	Pro	Trp			
106						120				125						130			
108	ttt	caa	cac	tat	cgg	aat	gtg	act	gtc	ggg	cct	cca	gaa	aac	att	gag		1089	
109	Phe	Gln	His	Tyr	Arg	Asn	Val	Thr	Val	Gly	Pro	Pro	Glu	Asn	Ile	Glu			
110						135				140						145			
112	gtg	acc	cca	gga	gaa	ggc	tcc	ctc	atc	atc	agg	ttc	tcc	tct	ccc	ttt		1137	
113	Val	Thr	Pro	Gly	Glu	Gly	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro	Phe			
114						150				155						160			
116	gac	atc	gtc	aat	acc	tcc	acg	gcc	ttt	ttt	tgt	tat	tat	gtc	cat	tac		1185	
117	Asp	Ile	Ala	Asp	Thr	Ser	Thr	Ala	Phe	Phe	Cys	Tyr	Tyr	Val	His	Tyr			
118						165				170						175			
120	tgg	gaa	aaa	gga	gga	atc	caa	cag	gtc	aaa	ggc	cct	ttc	aga	agc	aac		1233	
121	Trp	Glu	Lys	Gly	Gly	Ile	Gln	Gln	Val	Lys	Gly	Pro	Phe	Arg	Ser	Asn			
122						180				185						190		195	
124	tcc	att	tca	ttg	gat	aac	tta	aaa	ccc	tcc	aga	gtg	tac	tgt	tta	caa		1281	
125	Ser	Ile	Ser	Leu	Asp	Asn	Leu	Lys	Pro	Ser	Arg	Val	Tyr	Cys	Leu	Gln			
126						200				205						210			
128	gtc	cag	gca	caa	ctg	ctt	tgg	aac	aaa	agt	aac	atc	ttt	aga	gtc	ggg		1329	
129	Val	Gln	Ala	Gln	Leu	Leu	Trp	Asn	Lys	Ser	Asn	Ile	Phe	Arg	Val	Gly			
130						215				220						225			
132	cat	tta	agc	aac	ata	tct	tgc	tac	gaa	aca	atg	gca	gat	gcc	tcc	act		1377	
133	His	Leu	Ser	Asn	Ile	Ser	Cys	Tyr	Glu	Thr	Met	Ala	Asp	Ala	Ser	Thr			
134						230				235						240			
136	gag	ctt	cag	caa	gtc	atc	ctg	atc	tcc	gtg	gga	aca	ttt	tcg	ttg	ctg		1425	
137	Glu	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ser	Val	Gly	Thr	Phe	Ser	Leu	Leu			
138						245				250						255			
140	tcg	gtg	ctg	gca	gga	gcc	tgt	ttc	ttc	ctg	gtc	ctg	aaa	tat	aga	ggc		1473	
141	Ser	Val	Leu	Ala	Gly	Ala	Cys	Phe	Phe	Leu	Val	Leu	Lys	Tyr	Arg	Gly			
142						260				265						270		275	
144	ctg	att	aaa	tac	tgg	ttt	cac	act	cca	cca	agc	atc	cca	tta	cag	ata		1521	

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145	Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro Leu Gln Ile			
146	280	285	290	
148	gaa gag tat tta aaa gac cca act cag ccc atc tta gag gcc ttg gac	1569		
149	Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu Ala Leu Asp			
150	295	300	305	
152	aag gac agc tca cca aag gat gac gtc tgg gac tct gtg tcc att atc	1617		
153	Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val Ser Ile Ile			
154	310	315	320	
156	tcg ttt ccg gaa aag gag caa gaa gat gtt ctc caa acg ctt tga	1662		
157	Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr Leu			
158	325	330	335	
160	accaaaggcat gggcctagcc cactggctcc ctgaaagaga tcaaggccatc ggagctgcta	1722		
162	gagttctgtc tggacttcc agagaccagt atccctttt gctgcctcta aaaggcctgt	1782		
164	ccctgcacac atgagagaca gcaggctctca tgggggtgac aagctttttt ttttttttct	1842		
166	taaagaattt tcaaaatcaa attccagaat gatTTTACGG agatATCCCA ggaaaattaa	1902		
168	ggcttctctt aaacactaaa aaggcatgtt attgcttggt agcaaaatgg atatgacaca	1962		
170	tctctgatac ttttttcatt attgggtggg ctgagcagtc agaagacctg gtcgtcgct	2022		
172	tgactttggc aaatgagccg gagccccctt ggcaggcac acaacctgtc ccagcgaggg	2082		
174	acactgatgtt gcccattcatg tacatccatg gtgtgctggc ttaaaatgtt attaatctt	2142		
176	taaaatataact ccttagtaatt taagattttt tttttaaact ggaaataaaa gattgtatag	2202		
178	tgcatttttt tt	2214		
181	<210> SEQ ID NO: 4			
182	<211> LENGTH: 18			
183	<212> TYPE: DNA			
184	<213> ORGANISM: Artificial Sequence			
186	<220> FEATURE:			
188	<223> OTHER INFORMATION: PCR Primer			
190	<400> SEQUENCE: 4			
191	cagcaggctt cccaaatgg	18		
194	<210> SEQ ID NO: 5			
195	<211> LENGTH: 19			
196	<212> TYPE: DNA			
197	<213> ORGANISM: Artificial Sequence			
199	<220> FEATURE:			
201	<223> OTHER INFORMATION: PCR Primer			
203	<400> SEQUENCE: 5			
204	ggaggccccga cagtcacat	19		
207	<210> SEQ ID NO: 6			
208	<211> LENGTH: 28			
209	<212> TYPE: DNA			
210	<213> ORGANISM: Artificial Sequence			
212	<220> FEATURE:			
214	<223> OTHER INFORMATION: PCR Probe			
216	<400> SEQUENCE: 6			
217	tcaatgtcac tctacgcctt cgagctga	28		
220	<210> SEQ ID NO: 7			
221	<211> LENGTH: 19			
222	<212> TYPE: DNA			
223	<213> ORGANISM: Artificial Sequence			

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225 <220> FEATURE:
227 <223> OTHER INFORMATION: PCR Primer
229 <400> SEQUENCE: 7
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233 <210> SEQ ID NO: 8 19
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Primer
242 <400> SEQUENCE: 8
243 gaagatgggt atgggattc
246 <210> SEQ ID NO: 9 20
247 <211> LENGTH: 20
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Probe
255 <400> SEQUENCE: 9
256 caagcttccc gttctcagcc
259 <210> SEQ ID NO: 10 20
260 <211> LENGTH: 339
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
266 <400> SEQUENCE: 10
267 ttttagtoga aatgtttgct ttaatagccc ccaaagtaca tattaagctt tcaactctcc 60
269 cccgc(ccccc tccccctttt ttgagacgg agtcaccagg ctggagtgcgtggggcgat 120
271 ctccggctcac tgcaacctcc gcctccagtc aacccattt tgaaaagggt tttaaagggg 180
273 aggatgttaga aaggggcccg tgaaggagga ggtggggctc tgggggtggg gggaatggcc 240
275 tccgagcagg gggaggggaga gacagaaact tccagcattt ctaaatggcg tggggtttgc 300
277 cctggagccc gggcggtgc acgagtagga agtccctta 339
279 <210> SEQ ID NO: 11
280 <211> LENGTH: 54000
281 <212> TYPE: DNA
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <221> NAME/KEY: exon
286 <222> LOCATION: (514)...(1420)
287 <223> OTHER INFORMATION: Exon 1
289 <221> NAME/KEY: intron
290 <222> LOCATION: (1421)...(12692)
291 <223> OTHER INFORMATION: Intron 1
293 <221> NAME/KEY: exon
294 <222> LOCATION: (12693)...(12825)
295 <223> OTHER INFORMATION: Exon 2
297 <221> NAME/KEY: intron
298 <222> LOCATION: (12826)...(19284)
299 <223> OTHER INFORMATION: Intron 2

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301 <221> NAME/KEY: exon
302 <222> LOCATION: (19285)...(19490)
303 <223> OTHER INFORMATION: Exon 3
305 <221> NAME/KEY: intron
306 <222> LOCATION: (19491)...(24688)
307 <223> OTHER INFORMATION: Intron 3
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311 <223> OTHER INFORMATION: Exon 4
313 <221> NAME/KEY: intron
314 <222> LOCATION: (24838)...(29981)
315 <223> OTHER INFORMATION: Intron 4
317 <221> NAME/KEY: exon
318 <222> LOCATION: (29982)...(30141)
319 <223> OTHER INFORMATION: Exon 5
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322 <222> LOCATION: (30142)...(30518)
323 <223> OTHER INFORMATION: Intron 5
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326 <222> LOCATION: (30519)...(30676)
327 <223> OTHER INFORMATION: Exon 6
329 <221> NAME/KEY: intron
330 <222> LOCATION: (30677)...(34632)
331 <223> OTHER INFORMATION: Intron 6
333 <221> NAME/KEY: exon
334 <222> LOCATION: (34633)...(35318)
335 <223> OTHER INFORMATION: Exon 7
337 <400> SEQUENCE: 11
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339 gattacaggc gtgaggccacc gcgcctggca tcagtgcata ctttttgttgaag tgattccaag 120
340 ttatcgcccc cttttttcgt gtaacatata aatacatctc tgtatctaga aatatccaaat 180
341 gcataattca attgtctcg aggttattca tcacgtattt tcacgagcgt ggccaaatttc 240
342 aaaatagttc tacaaagagg aaatgcaaga atgtgggaag agcaaaaagaa aagctctatg 300
343 ttgcaaaaacc catttttgct aacgtgtcca gtgggctccc gggacgaccc ttttttaaat 360
344 tcttggtctc cctgcaccgc gtccttcctt tgctgcgcta gctttatgac gcattttgg 420
345 agaacaggcc agatttaaaa ccctctccca acaggcgtca aacgacatgg tgcaggctcg 480
346 ggctggggag cgggcctcg gctgcccagc tgctaaagga ctccctactc gtgcaccgcc 540
347 gccggctcca gggcaaaaccc cacgcattt agaaatgtctg gaagtttctg tctctccctc 600
348 cccctgctcg gagggcattt ccccccccccc cagagccccca cctccctt cactggggcc 660
349 ttcttaactc ctteccctta aaaccctttt caaaatgggg ttgactggag gcgaggttg 720
350 cagtgagccg agatcggccc actgcactcc agcctggta ctccgtctca aaaaaaaagg 780
351 gagggggggcg ggggagagtt gaaagctta tatgtacttt gggggctatt aaagcaaaca 840
352 ttgcactaa aggggcaat cctcgaattt tgcatcaag caccggagag gagatgggg 900
353 gggggtcagg aggggtgggg gctccaggga aagccccgggg gtctggccg gggctcg 960
354 gggcccttcc ggaaggatcg cggccccca aggtgggcgt cccgcgggac tccagtctcc 1020
355 aggacgttcc gggaggctcc gcgcctggg aggcggctg cgtgggtcc cgcgcgtca 1080
356 gcccgcaggc cccccccaggc cccgcgttcc cggagcggga aagtcccgccg cggggggcg 1140
357 ggcctcgggg gccccacggg ggggggggggg gggcgccgggc ggcgcggccg aatccccctcc 1200
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/843,377

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Input Set : A:\RTS-0235 Sequence Listing.txt
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date